

**CRF Errors Edited by the STIC Systems
Branch**

Serial Number: 10/070, 794A

CRF Edit Date: 1/9/04
Edited by: KE

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

ENTERED

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

___ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

✓ Other:

Deleted numbering for two
stop codons, not intended, for
Seq IDs 27, 29.



PCT

RAW SEQUENCE LISTING

DATE: 01/09/2004

PATENT APPLICATION: US/10/070,794A

TIME: 12:09:35

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\01092004\J070794A.raw

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4 <110> APPLICANT: ANDERSSON, Leif
5      LOOFT, Christian
6      KALM, Ernst
7      MILAN, Denis
8      ROBIC, Annie
9      ROGEL-GAILLARD, Claire
10     IANNUCELLI, Nathalie
11     GELLIN, Joel
12     LE ROY, Pascale
13     CHARDON, Patrick
15 <120> TITLE OF INVENTION: VARIANTS OF THE GAMMA CHAIN OF AMPK, DNA SEQUENCES ENCODING
16     THE SAME, AND USES THEREOF
18 <130> FILE REFERENCE: 11145-023US1
20 <140> CURRENT APPLICATION NUMBER: US 10/070,794A
C--> 21 <141> CURRENT FILING DATE: 2003-05-23
23 <150> PRIOR APPLICATION NUMBER: PCT/EP00/09896
24 <151> PRIOR FILING DATE: 2000-09-11
26 <150> PRIOR APPLICATION NUMBER: EP 00401388.4
27 <151> PRIOR FILING DATE: 2000-05-18
29 <150> PRIOR APPLICATION NUMBER: EP 99402236.3
30 <151> PRIOR FILING DATE: 1999-09-10
32 <160> NUMBER OF SEQ ID NOS: 42
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35 <211> LENGTH: 1867
36 <212> TYPE: DNA
37 <213> ORGANISM: Sus scrofa
39 <220> FEATURE:
40 <221> NAME/KEY: CDS
41 <222> LOCATION: (472)..(1389)
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46 agaagccatg gggaccaggg gaacaaggcc tctagatgga caaggcagga ggatgtagag 120
48 gaaggggggc ctccggggcc gaggaaggt cccaggtcca ggccagttgc tgagtccacc 180
50 gggcaggagg ccacattccc caaggccaca cccttgccc aagccgtcc cttggccgag 240
52 gtggacaacc cccaacaga gcgggacatc ctcccctctg actgtgcagc ctcagcctcc 300
54 gactccaaca cagaccatct ggatctgggc atagagttct cagcctcggc ggcgtcgggg 360
56 gatgagcttg ggctggtgga agagaagcca gcccgtgcc catcccaga ggtgctgtta 420
58 ccaggctggt gctgggatga tgagctgcag aagccggggg ccagggtcta c atg cac 477
59                                     Met His
60                                     1
62 ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc aaa 525
63 Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser Lys
64                                     5                10                15

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70 ctg gtg gcc aac ggc gtc cga gcg gca cct ttg tgg gac agc aag aag 621
71 Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys Lys
72 35                      40                      45                      50
74 cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg ctg 669
75 Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val Leu
76      55                      60                      65
78 cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa gaa 717
79 His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu Glu
80      70                      75                      80
82 cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc aag 765
83 His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe Lys
84      85                      90                      95
86 cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc tac 813
87 Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val Tyr
88      100                      105                      110
90 gcc ctc atc aag aac cgg atc cac cgc ctg ccg gtc ctg gac cct gtc 861
91 Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro Val
92 115                      120                      125                      130
94 tcc ggg gct gtg ctc cac atc ctc aca cat aag cgg ctt ctc aag ttc 909
95 Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys Phe
96      135                      140                      145
98 ctg cac atc ttt ggc acc ctg ctg ccc cgg ccc tcc ttc ctc tac cgc 957
99 Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr Arg
100      150                      155                      160
102 acc atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg gtg 1005
103 Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val Val
104      165                      170                      175
106 ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc gtg gac cgg 1053
107 Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp Arg
108      180                      185                      190
110 cgt gtg tct gcg ctg cct gtg gtc aac gaa act gga cag gta gtg ggc 1101
111 Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val Gly
112 195                      200                      205                      210
115 ctc tac tct cgc ttt gat gtg atc cac ctg gct gcc caa caa aca tac 1149
116 Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr Tyr
117      215                      220                      225
119 aac cac ctg gac atg aat gtg gga gaa gcc ctg agg cag cgg aca ctg 1197
120 Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr Leu
121      230                      235                      240
123 tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg gaa 1245
124 Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly Glu
125      245                      250                      255
127 gtc att gac cgg att gtc cgg gaa cag gtg cac cgc ctg gtg ctc gtg 1293
128 Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu Val
129      260                      265                      270
131 gat gag acc cag cac ctt ctg ggc gtg gtg tcc ctc tct gac atc ctt 1341

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133 275                280                285                290
135 cag gct ctg gtg ctc agc cct gct gga att gat gcc ctc ggg gcc tga 1389
136 Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
137                295                300                305
139 gaaccttgga acctttgctc tcaggccacc tggcacacct ggaagccagt gaagggagcc 1449
141 gtggactcag ctctcacttc ccctcagccc cacttgctgg tctggctctt gttcaggtag 1509
143 gctccgccc gggccctgg cctcagcatc agcccctcag tctccctggg caccagatc 1569
145 tcagactggg gcaccctgaa gatgggagt gcccagctta tagctgagca gcctgtgaa 1629
147 atctaccagc atcaagactc actgtgggac cactgctttg tcccattctc agctgaaatg 1689
149 atggagggcc tcataagagg ggtggacagg gcctggagta gaggccagat cagtgcagt 1749
151 ccttcaggac ctccggggag ttagagctgc cctctctcag ttcagttccc ccctgctgag 1809
153 aatgtccctg gaaggaagcc agttaataaa ccttggttgg atggaatttc cacactcg 1867
156 <210> SEQ ID NO: 2
157 <211> LENGTH: 305
158 <212> TYPE: PRT
159 <213> ORGANISM: Sus scrofa
161 <400> SEQUENCE: 2
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163 1 5 10 15
165 Ser Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe
166 20 25 30
168 Phe Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser
169 35 40 45
172 Lys Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu
173 50 55 60
175 Val Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile
176 65 70 75 80
178 Glu Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys
179 85 90 95
181 Phe Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala
182 100 105 110
184 Val Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp
185 115 120 125
187 Pro Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu
188 130 135 140
190 Lys Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu
191 145 150 155 160
193 Tyr Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala
194 165 170 175
196 Val Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val
197 180 185 190
199 Asp Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val
200 195 200 205
202 Val Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln
203 210 215 220
205 Thr Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg
206 225 230 235 240
208 Thr Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu

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209          245          250          255
211 Gly Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val
212          260          265          270
214 Leu Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp
215          275          280          285
217 Ile Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly
218          290          295          300
220 Ala
221 305
225 <210> SEQ ID NO: 3
226 <211> LENGTH: 2109
227 <212> TYPE: DNA
228 <213> ORGANISM: Homo sapiens
230 <220> FEATURE:
231 <221> NAME/KEY: CDS
232 <222> LOCATION: (472)..(1389)
234 <400> SEQUENCE: 3
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239 gaagggggagc caccaggtca gggggaaggt ccccggtcca ggccaactgc tgagtccacc 180
241 gggctggagg ccacattccc caagaccaca cccttggtc aagctgatcc tgccgggggtg 240
243 ggcactccac caacagggtg ggactgcctc ccctctgact gtacagcctc agctgcaggc 300
245 tccagcacag atgatgtgga gctggccacg gagttcccag ccacagaggc ctggggagtgt 360
247 gagctagaag gcctgctgga agagaggcct gccctgtgcc tgtccccgca ggccccattt 420
249 cccaagctgg gctgggatga cgaactgcgg aaaccggcg cccagatcta c atg cgc 477
250                                     Met Arg
251                                     1
253 ttc atg cag gag cac acc tgc tac gat gcc atg gca act agc tcc aag 525
254 Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser Lys
255          5          10          15
257 cta gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt gct 573
258 Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe Ala
259          20          25          30
261 ctg gtg gcc aac ggt gtg cgg gca gcc cct cta tgg gac agc aag aag 621
262 Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys Lys
263          35          40          45          50
265 cag agc ttt gtg ggg atg ctg acc atc act gac ttc atc ctg gtg ctg 669
266 Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val Leu
267          55          60          65
269 cat cgc tac tac agg tcc ccc ctg gtc cag atc tat gag att gaa caa 717
270 His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu Gln
271          70          75          80
273 cat aag att gag acc tgg agg gag atc tac ctg caa ggc tgc ttc aag 765
274 His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe Lys
275          85          90          95
277 cct ctg gtc tcc atc tct cct aat gat agc ctg ttt gaa gct gtc tac 813
278 Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val Tyr
279          100          105          110
281 acc ctc atc aag aac cgg atc cat cgc ctg cct gtt ctt gac ccg gtg 861

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TIME: 12:09:35

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282 Thr Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro Val
283 115 120 125 130
286 tca ggc aac gta ctc cac atc ctc aca cac aaa cgc ctg ctc aag ttc 909
287 Ser Gly Asn Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys Phe
288 135 140 145
290 ctg cac atc ttt ggt tcc ctg ctg ccc cgg ccc tcc ttc ctc tac cgc 957
291 Leu His Ile Phe Gly Ser Leu Leu Pro Arg Pro Ser Phe Leu Tyr Arg
292 150 155 160
294 act atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gct gtg gtg 1005
295 Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val Val
296 165 170 175
298 ctg gag aca gca ccc atc ctg act gca ctg gac atc ttt gtg gac cgg 1053
299 Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp Arg
300 180 185 190
302 cgt gtg tct gca ctg cct gtg gtc aac gaa tgt ggt cag gtc gtg ggc 1101
303 Arg Val Ser Ala Leu Pro Val Val Asn Glu Cys Gly Gln Val Val Gly
304 195 200 205 210
306 ctc tat tcc cgc ttt gat gtg att cac ctg gct gcc cag caa acc tac 1149
307 Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr Tyr
308 215 220 225
310 aac cac ctg gac atg agt gtg gga gaa gcc ctg agg cag agg aca cta 1197
311 Asn His Leu Asp Met Ser Val Gly Glu Ala Leu Arg Gln Arg Thr Leu
312 230 235 240
314 tgt ctg gag gga gtc ctt tcc tgc cag ccc cac gag agc ttg ggg gaa 1245
315 Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Ser Leu Gly Glu
316 245 250 255
318 gtg atc gac agg att gct cgg gag cag gta cac agg ctg gtg cta gtg 1293
319 Val Ile Asp Arg Ile Ala Arg Glu Gln Val His Arg Leu Val Leu Val
320 260 265 270
322 gac gag acc cag cat ctc ttg ggc gtg gtc tcc ctc tcc gac atc ctt 1341
323 Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile Leu
324 275 280 285 290
326 cag gca ctg gtg ctc agc cct gct ggc atc gat gcc ctc ggg gcc tga 1389
327 Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
328 295 300 305
330 gaagatctga gtcctcaatc ccaagccaac tgcacactgg aagccaatga aggaattgag 1449
332 aacagcttca tttccccaac cccaatttgc tggttcagct atgattcagg cttcttcagc 1509
334 cttccaaaat tgcctttgcc ttacttgtgc tcccagaacc cttcgggcat gccagtgca 1569
336 ccatgggatg atgaaattaa ggagaacagc tgagtcaagc ttggaggtcc ctgaaccaga 1629
338 ggcactagga ttaccccagg gccatctgtg ctccatgccc gcccatcccc ttgccgctg 1689
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356 <211> LENGTH: 305

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/070,794A

DATE: 01/09/2004

TIME: 12:09:36

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\01092004\J070794A.raw

L:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date